

GenCore version 5.1.4 ps_4578
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OK nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:16:08 ; Search time 4340.53 Seconds

(without alignments)
10982.631 Million cell updates/sec

Title: US-09-001-737-7_COPY_15_1652

Perfect score: 1638

Sequence: 1 ATGCCAAGAAATCAAAAT.....TCGGTGGATGCGCGGATTA 1638

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402678 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank :
1: gb_ba :
2: gb_hg :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pat :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sts :
12: gb_sy :
13: gb_un :
14: gb_vl :
15: em_ba :
16: em_fun :
17: em_in :
18: em_mu :
19: em_om :
20: em_ov :
21: em_ph :
22: em_pat :
23: em_pl :
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41: em_vl :
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45: em_vl :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1620.2	98.9	10389	1	AE006627
2	1605.8	98.0	53291	1	AE014170
3	1602.6	97.8	11576	1	AE010115
4	1413.4	86.3	2683	6	SPGROELGN
5	1413.4	86.3	2683	6	AX148805
6	1170.4	71.5	1421	1	AX121365
7	1140.4	69.6	1421	6	AX148806
8	1128.8	68.9	1421	1	AX121364
9	1125	68.7	1422	1	AX121366
10	1122.6	68.5	1305	6	AX148809
11	1118	68.3	1425	1	AX121367
12	1104.2	67.4	2024	1	AX121368
13	1073.4	65.9	1384	1	AX121369
14	1073.4	65.7	2324	1	AX389516
15	1068.2	65.2	2320	1	AX389515
16	1063.6	64.9	2020	1	AX389517
17	1052.8	64.3	1718	1	AF328222
18	1050.4	64.1	2639	1	AF378195
19	1039.2	63.4	1623	6	AX194119
20	1038.4	63.4	1926	6	AX073958
21	1037.6	63.3	21494	2	SPNEU1924
22	1036	63.2	1647	6	AX194338
23	1036	63.2	2107	6	AF325449
24	1036	63.2	2107	6	AX148804
25	1034.4	63.2	5365	6	BD003757
26	1034.4	63.2	11318	1	AE008538
27	1034.4	63.2	13103	1	AE007482
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29	1029.6	62.9	2401	6	AX148802
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31	1012.4	61.8	2480	1	AF378197
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45	821.6	50.2	295050	1	AL591982

ALIGNMENTS

RESULT 1
LOCUS AE006627 10389 bp DNA linear BCT 01-JUN-2001
DEFINITION Streptococcus pyogenes M1 GAS strain SF370, section 156 of 167 of
the complete genome.
ACCESSION AE006627 AE004092
VERSION AE006627.1 GI:13623059
KEYWORDS
SOURCE Streptococcus pyogenes M1 GAS.
ORGANISM Streptococcus pyogenes M1 GAS.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE
1 (bases 1 to 10389)
Ferretti J.J., McShan W.M., Adjuic D., Savic G., Lyon K.,
Primeaux C., Seaton S.S., Surov A.N., Kenton S., Lal H., Lin S.,

TITLE	Qian, X., Jia, H.G., Najjar, F.Z., Ren, O., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E. Complete genome sequence of an M1 strain of <i>Streptococcus pyogenes</i> Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
JOURNAL	2192684
MEDLINE	11296296
PUBMED	2 (bases 1 to 10389)
AUTHORS	Perreletti, J.J., McShan, W.M., Adjic, D., Savic, D., Savic, G., Lyon, R., Pineaux, C., Szate, S.S., Surovov, A.N., Kenton, S., Lai, H., Lin, S., Qian, X., Jia, H.G., Najjar, F.Z., Ren, O., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E. Direct Submission Submitted (10-APR-2001) Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940. St Young Blvd, Oklahoma City, OK 73104, USA
FEATURES	Location/Qualifiers 1..10389
SOURCE	/organism="Streptococcus pyogenes M1 GAS" /strain="SP370" /serotype="M1" /db_xref="taxon:160490" complement(75..1799) /gene="SPY2065" .1799) complement(75..1799) /note="Best Blastp hit = prf112109195A chondroitin ABC lyase [Proteus vulgaris]" /codon_start=1 /transl_table=1 /product="hypothetical protein" /protein_id="AAK34725.1" /db_xref="GI:13623060" /translation="MYLGFENPFLAYDIIVKKNIESMGLMKPPHKKIKOTIT AATSLFELIGAYYSKHNHCINAYLKARSQSPVENIKAYLVMDNDRITNDRA MYTFRRYSOKELROKODKAAQSODSAYOVKSVGRFRIFPDRIALIKPHITIKTN VPOADVLNOKKAVSDSDFSVKLDRLPAETTAISIRKNGKNGIKVKSIDQDNV LDLSVFRPLVPLVSNAGDLEFDNHNIGLKKOLOYEDPYPTENAKVAKTTPG ELRSOKVALADVEGATLEILWDLIEDNAGLISAPDLNHTISTQDSSNRYE FEESGNAFYGLKESKAPOTPRKASPLNPSILITLITVOKTIVLDFPVS FLYKSTDEPHQTSGLNODLQVYKRGKQHTLISOSGSKITVAKEDNKLAPV FPESLITGANGSISMSLASGITTTTRVEDOKRSKERTAKISKEDGNF VLTTPRGSDLSALVEGGLGANKATAYFKISGTASPVWQALTHEEDYTKPLS GVTLAKOP"
gene	1962..3458
CDS	/gene="SPY2065" 1962..3458 /note="Best Blastp hit = emb1CA66893.1 (X98238) putative: orf1 [lactobacillus sakei]" /codon_start=1 /transl_table=1 /product="putative dipeptidase" /protein_id="AAK34726.1" /db_xref="GI:13623061" /translation="MINKKISGLVITTFASISQSVACHTGCTICKDITOGSLLYG FREDLEPHNNKNTVILAKNDPAGERKDSNGFTYPPENSTRISALPDVTAPKGYV DAGNEFGYSNATYSANDAIQKIDPVNGLAESMSVILPSTVTAEBGVALI AKIVEKGAECVITLADKQITMELISGQVYALPDDYAVAVPTVYLDGHDV NKEKNTIASDEVKAKKASTITVDKRTIAKSTNPDLNDRSSSGISLDPDS KTYVQDSNTELDSTKRTFLEDMKLDORREGLDLPLDQALDGSKSSGSKKAV GATVTSNPMWNAHIFOLKQDITAEIGVWMLSGSRNAPLPLAIGNISRTYEAQ EKSTYINOKSWTVSHINDLVAAHPPPGTIVIDENKGLKWTVAEDKSTKESIDL VSDPKAOKERADKISLDRAKTKTKRLKAIEAKLVKEKPNKKGLNRS" complement(4661..6292) /gene="gi061" /note="SPY2070" complement(4661..6292) /gene="gi061" /note="The N-terminal amino acid sequence of this ORF has been determined from a spot isolated by 2-D gel electrophoresis from another strain of <i>S. pyogenes</i> , Hogan, D. A., Whittom, M. M., Rogers, J. and R. A. VanBogelen, 2000. Two-dimensional gel electrophoresis map of
gene	618..6618
CDS	/gene="SPY2072" complement(6328..6618) /gene="gi061" complement(6328..6618) /note="The N-terminal amino acid sequence of this ORF has been determined from a spot isolated by 2-D gel electrophoresis from another strain of <i>S. pyogenes</i> , Hogan, D. A., Whittom, M. M., Rogers, J. and R. A. VanBogelen, 2000. Two-dimensional gel electrophoresis map of <i>Streptococcus pyogenes</i> proteins. Unpublished data. Best Blastp hit = gblAA75592.1(AZ214488.2 (AF214488) GroES [lactobacillus johnsonii]" /codon_start=1 /transl_table=1 /product="heat shock protein - co-chaperonin" /protein_id="AAK34728.1" /db_xref="GI:13623063" /translation="MLKPLGRVAVFDEKEQVGFVLAQTKESTRAVAVASE TGVTITGGSVLPVSVOGEVLENGHLEVTVDKVSIIRESDIATVTK" complement(6796..9240) /gene="clpC" /note="SPY2073" complement(6796..9240) /gene="clpC" /note="Best Blastp hit = gblAAC4446.1 (U0604) ClpC [Bacillus subtilis monocytoenes]" /codon_start=1 /transl_table=1 /product="putative endopeptidase Clp ATP-binding chain C" /protein_id="AAK34729.1" /db_xref="GI:13623064" /translation="MIVSTKMDIFRQAFQFARFDSHCLTWHVLLAVVNDLSIA NMLISYDAOVAIEVEAAILAMKQTPKPEQLSRVFPKQSTLNLVAFALASOT RDEQSEHVLFAILLNPIDMASRLLEIAGIYQKDNQNGOQLRLAKRAIEHAGYSK EMKAIHEIRKRTKKTGCGFESDMKPPSAGLSQFRLDEAROGLESVIGRDO EVRMIOVSRKTNPNVLCVAGAGKALAYLALORANADYELKEMKRLTIDLM SVAGRFGDFEERNMIDIDLEDOGLITFVDELHTFMSSGDIQALMGKISYPT YHNSISNAAVTAVKARHAYLSNLSADAILDLDEKSAVONKRAVQIMGLKISYPT QALINDMKKVSRLAKKQMRPPTVYEDITLITKSGISCIPEKRTQADSKKL NLKELHKKVIGODAAVTAISRAITRNSGIPRQGRPVYDGSCEGLORVANKRTVLA NEVLFDEALIRFDMSEWEMKPAASUNAPKPGVYDGSCEGLORVANKRTVLA DEKRAHIDFNVLVDGLDGLTDSGRKRVDSNTIITNSIKGALADKTVGG VKIHOHDAEMKRTIPELRKTYRPTINIDKRVVSHLSQNDMDVVKIMVPLT TLAKRGITLKIOPALKHLSEVIGIDHMGARPLRLDTETELKSELITLSHETSCH TLKIGLSHKTIFHIA
gene	9240..9701
CDS	/gene="clpR" complement(9240..9701) /note="SPY2074" complement(9240..9701) /gene="clpR" /note="Best Blastp hit = sp1P375681C7SR_BACSU TRANSCRIPTIONAL REULATOR CTRR -gbl12170521P111566112 transcription repressor ctsr - Bacillus subtilis

				>gl46747 dbj BAO05317.1 (D26185) unknown [Bacillus subtilis] >gl1263250 emb CAI1859.1 (t29104)* transcripiional regulator [Bacillus subtilis]*
			/codon_start=1	
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			/transl_table=11	
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			/db_xref="GI:13623065"	
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	gene		/complement(9897...10100)	
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BASE COUNT	3077	a	2210 c	1855 g 3247 t
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Query Match	98.9%	Score 1620.2:	DB 1;	Length 10389;
Best Local Similarity	99.8%;	Pred. No. 0;	Mismatches 3;	Indels 0;
Matches 1632:	Conservative 0;	Gaps 0;		
Oy	I	ATGCCAAGAATCAAAATTTCACGAGTAGTGCGCTGCATCATGTGCGCCGAAGTGAT	60	
Db	6292	ATGCCAAAAGATTTAAATTTCACGAGTAGTGCGCTGCATCATGTGCGCCGAAGTTAT	6233	
Oy	61	ATGTTAGCAGATCGCTCAAGTAAGACTGCTGCTTAAAGSCGAATGTGTTCTTGAA	120	
Db	6232	ATGTTAGCAGATCGCTCAAGTAAGACTGCTGCTTAAAGSCGAATGTGTTCTTGAA	6173	
Oy	121	AAGCTTTGGTTCOCCTTAATTAATATGACGGGGTAACCATTGCTTAAGATGAA	180	
Db	6172	AAAGCTTTGGTTCOCCTTAATTAATTAATGACGGGGTAACCATTGCTTAAGATGAA	6113	
Oy	181	TTAGAAGATCAATTTGAAAAACATGGAGAACAAATGTGTCCTGAAGTGGCTTTAAAC	240	
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Oy	241	AATGATATTCGTGTGATGGAGCACTACTGCAACAATTTGACACAAGCAATTTGCAT	300	
Db	6052	AATGATATTCGTGTGATGGAGCACTACTGCAACAATTTGACACAAGCAATTTGCAT	5993	
Oy	301	GAAAGACTAAAAAATGTGACAGCAGGTGCTATCCAATTTGATATCCATGAGACATTGA	360	
Db	5992	GAAAGACTAAAAAATGTGACAGCAGGTGCTATCCAATTTGATATCCATGAGACATTGA	5933	
Oy	361	ACAGCAACACCAACAGCTGTGTAAGCTTTGAAGCACATTGCTCAACCTGATCTGGCA	420	
Db	5932	ACAGCAACACCAACAGCTGTGTAAGCTTTGAAGCACATTGCTCAACCTGATCTGGCA	5873	
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Oy	481	TCAGAACTCTGAGACGTGTGGGCAAGATGTGTATTAACATCGAATAATCTCGAGCT	540	
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Db	5752	ATGGAAACAGAACTGAAGTGTTGAAGCATTCGAATTTGACGCTGTTACTGTCTCAA	5693	
Oy	601	TTCATGTCTACAGCATGAAAAATGCTTGACAGACTTTGAAAAACCATTTATCTTATC	660	

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Qy	721	ACCAACCGTCATTACTATTTATGACAGATGATGSGATGSGTAAACACTTCACACCTT	780
Db	5572	ACCAACCGTCATTACTATTTATGACAGATGATGSGATGSGTAAACACTTCACACCTT	5513
Qy	781	GCTTGACCAAGATGTTGGTGTCTTAAATGAGGTTGCTGTCAACGCCAGATTGGT	840
Db	5512	GCTTGACCAAGATGTTGGTGTCTTAAATGAGGTTGCTGTCAACGCCAGATTGGT	5453
Qy	841	GATCGCCCTAAAGCTATGCTTGAAGACATTCCTTGAACGTTGACAGTGTATTA	900
Db	5452	GATCGCTGTAAGATATGCTTGAAGACATTCCTTGAACGTTGACAGTGTATTA	5393
Qy	901	GAGGATCTGAGACTTGAATTAAGATGCTACAAATGACAGCCCTTGACAGCGTGA	960
Db	5392	GAGGATCTGAGACTTGAATTAAGATGCTACAAATGACAGCCCTTGACAGCGTGA	5333
Qy	961	ATTACGTTGATAAAGATAGCAGCAGTAATTTGTTGAAGTTTCAGAAAGTTCAAGAT	1020
Db	5332	ATTACAGTTGATAAATAGCAGCAGTAATTTGTTGAAGTTTCAGAAAGTTCAAGAT	5273
Qy	1021	GCTAACCTATTATCAGTATTAATTCACAAATTAAGAAACAACACTTCGATTTGACGT	1080
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Qy	1141	GCTCAACAGAGACACTTAAAGAAATGAACCTGCGCAATGAGATGCTCTAAATGCT	1200
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Qy	1201	ACACGTCAGCCCTGAAGAAAGATATGCTGCTGGTGGTGAGACAGACTTATACGTT	1260
Db	5092	ACACGTCAGCCCTGAAGAAAGATATGCTGCTGGTGGTGAGACAGACTTATACGTT	5033
Qy	1261	ATTGAAAAAGTAGACAGCTCTTGAGCTTGAAGGGCAGTATGCTACAGCAATATGTG	1320
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Qy	1321	CTTCTGTGCTAGAGACCTGTACGTCAAAATTCCTTAAAGTGTGGGTACGAAGGCTCC	1380
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Db	4912	GTAGTATTATACAAAGTTGAAGAAACACCCCTCAGAGAAAGAAATTAATGCTCAACAGT	4853
Qy	1441	GAGTGGTATATGATTAAGAAACAGAAATCATATACCGTGAAGAAATTAACAGATCAGC	1500
Db	4852	GAGTGGTATATGATTAAGAAACAGAAATCATATACCGTGAAGAAATTAACAGATCAGC	4793
Qy	1501	CTTCAAAATGACAGCTTCGTAAGGTATCTTATTTGACACAGAAAGAGTTGGTCTAAT	1560
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Qy	1561	AAACCTAACACAGCTACGCCAGCGCCAGCAATGCAACAGAGATATGATCCAGAAATGATG	1620
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AE014170/c	AE014170	53291 bp	DNA	11 linear	BCT 19-JUL-2002
LOCUS	Streptococcus pyogenes MGAS315, section 35 of 37 of the complete genome.				
DEFINITION	AE014170 AE014074				
ACCESSION	AE014170.1 GI:21905475				
VERSION					
KEYWORDS					
SOURCE	Streptococcus pyogenes MGAS315.				
ORGANISM	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.				
REFERENCE	1 (bases 1 to 53291)				
AUTHORS	Beres, S.B., Sylva, G.L., Barblian, K.D., Lei, B., Hoff, J.S., Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F., Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and Musser, J.M.				
TITLE	Genome sequence of a serotype M3 strain of group A Streptococcus: Phage-encoded toxins, the high-virulence phenotype, and clone emergence.				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)				
REFERENCE	2 (bases 1 to 53291)				
AUTHORS	Beres, S.B., Sylva, G.L., Barblian, K.D., Lei, B., Hoff, J.S., Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F., Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and Musser, J.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-JUN-2002) Laboratory of Human Bacterial Pathogenesis, Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St., Hamilton, MT 59840, USA				
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LOCUS Streptococcus pyogenes strain MGS8232, section 163 of the
DEFINITION complete genome
ACCESSION AE010115 AE009949
VERSION AE010115.1 GI:19749196
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SOURCE Streptococcus pyogenes MGS8232.
ORGANISM Streptococcus pyogenes MGS8232.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 11576)
AUTHORS Smoot,J.C., Barbican,K.D., Van Gompel,J.J., Smoot,L.M.,
Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.,
Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks
Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)
2 (bases 1 to 11576)
JOURNAL Smoot,J.C., Barbican,K.D., Van Gompel,J.J., Smoot,L.M.,
MEDLINE Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
PUBLISHED Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,
11917108 Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.,
Direct Submission
TITLE Submitted (31-JAN-2002) Laboratory of Human Bacterial
JOURNAL Pathogenesis/Rocky Mountain Laboratories/NIH/NIH, 903 S. 4th St.,
Hamilton, MT 59840, USA
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Dd	2106	ATGTTAGCAGATACCGGTGAAGTAACGCTTGGTCTTAAGGGCGCATGTTGTTCTGAA	2047
OY	121	AAAGCTTTGGTTCCTCTTAATTACTATACAGGGGTAAACCATGCTTAAAGAGATGAA	180
Dd	2046	AAAGCTTTGGTTCCTCTTAATTACTATACAGGGGTAAACCATGCTTAAAGAGATGAA	1987
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Dd	1566	TACATGGTCAAGCAATGAAGAAATGGTTCGACAGCTTGAAGAACCATTTATCTTAAATC	1507
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Dd	1386	GCTTTGAACAAGATTGCTGCTACTTTCAAATGGTGGTGTCTCAAAAGCCCAAGATTTGGT	
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us-09-001-737-7_copy_15_1652.rge

Authors	Journal	Comment	Related sequences	Location/Qualifiers
John B. Poddielecki, A. and Zargen, I.	Unpublished	Related sequences M8132, M84965.	Location/Qualifiers	1. 2683
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BASE COUNT		593 g	792 t	
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			0	Indels
			0	Gaps
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0y	247	ATTGCTGGTATGCGACGACACTCTGACAGATTTTGGACAAAGCCATTGTCTGATGAGCA	306	
Db	61	ATTGCTGGTATGCGACGACACTCTGACAGATTTTGGACAAAGCCATTGTCTGATGAGCA	120	
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0y	427	ATTGCTAGGTGGCTGACAGTATCATACGCTCTGAAAAAGTTGAGAGATATATCTCAGAA	486	
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0y	667	AAAAAATGTGCAACATCTCAAGACATTTGGCACTACTTGAAGAAAGTCTTTAAACCAAC	726	
Db	481	AAAAAATGTGCAACATCTCAAGACATTTGGCACTACTTGAAGAAAGTCTTTAAACCAAC	540	

AUTHORS		TITLE		JOURNAL		FEATURES		BASE COUNT		ORIGIN	
Wright, J. A., Young, A. H., and Dugourd, D.		Antisense oligonucleotide sequences derived from groEL and groES genes of <i>Escherichia coli</i>		Inhibitors of microorganisms Patent: WO 0136525-A 7 25-MAY-2001; Genesense Technology Inc. (CA)		Location/Qualifiers 1, 2683		/organism="Streptococcus pyogenes" /db_xref="taxon:1314"		808 a 490 c 593 g 792 t	
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Oy	307	CTAAATAATGTGACAGCAGGCGCTATCCATATTTGTTATCCGTCGAGCAGCATTTGAACACA	366								
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RESULT 6
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DEFINITION Streptococcus dysgalactiae subsp. equisimilis strain ATCC 12394
ACCESSION AY121365
VERSION AY121365.1 GI:22022489
KEYWORDS
SOURCE Streptococcus dysgalactiae subsp. equisimilis.
ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 1421)
AUTHORS Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,
Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
TITLE Characterization of the gene of group G Streptococcus dysgalactiae
JOURNAL subsp. equisimilis
REFERENCE unpublished
AUTHORS 2 (bases 1 to 1421)
Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,
Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
Pokfulam Road, Hong Kong, China
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BASE COUNT 417 a 273 c 354 g 377 t
ORIGIN

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Oy 551 AACTTGAAGTGTGAAGCATGCAATTTGACCGTGTGATGATGATGATGATGATGATG 610
Db 481 AACTTGAAGTGTGAAGCATGCAATTTGACCGTGTGATGATGATGATGATGATGATG 540
Oy 611 CAGACAAAGAAAATGTTGACGACCTGAAACCCATTTATCTTGATTCAGATATAA 670
Db 541 CAGACAAAGAAAATGTTGACGACCTGAAACCCATTTATCTTGATTCAGATATAA 600
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Oy 731 CATTAATCATTAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 790
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Oy 851 AAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 910

Db 781 AGCTATGCTGAGACATCTCTATCTTGACAGGCTGTACAGGATACAGAGATCTAG 840
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RESULT 7
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LOCUS AX148806
DEFINITION Sequence 8 from Patent WO136625.
ACCESSION AX148806
VERSION AX148806.1 GI:14347330
KEYWORDS
SOURCE Streptococcus pyogenes.
ORGANISM Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 1306)
AUTHORS Wright,J.A., Young,A.H. and Dugourd,D.
TITLE Inhibitors of oligonucleotide sequences derived from groEL and groES as
inhibitors of microorganisms
JOURNAL Patent: WO 0136625 A 8 25-MAY-2001;
Genesense Technologies Inc. (CA)
FEATURES
Location/Qualifiers
Source 1..1306
/organism="Streptococcus pyogenes"
/db_xref="taxon:1314"
BASE COUNT 407 a 235 c 308 g 356 t
ORIGIN

Query Match 69.6%; Score 1140.4; DB 6; Length 1306;
Best Local Similarity 99.9%; Pred. No. 6.3e-223;
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 664 GATAAAGATGTCAACATCCAGACATTTTGCACACTTGTGAGAGATGTTAAGC 723
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Db 302 TTGACAGAAATGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
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Db 362 CCGTGAAGCTATGCTTGAAGACATTTGCTATCTTGAAGAGTGTACAGTATTAAGAG 421
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Page 12

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Db 1142 GG 1143

RESULT 8
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LOCUS AY121364
DEFINITION Streptococcus dysgalactiae subsp. equisimilis strain ATCC 35666
ACCESSION AY121364
VERSION AY121364.1 GI:22022487
KEYWORDS
SOURCE Streptococcus dysgalactiae subsp. equisimilis.
ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
REFERENCE 1 (bases 1 to 1421)
AUTHORS Woo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. W.,
Tse, H., Mong, K. -L., Li, K. -W., Lam, K. -C. and Yuen, K. -Y.
TITLE Streptococcus dysgalactiae subsp. equisimilis strain ATCC 35666
JOURNAL Unpublished
AUTHORS Woo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. W.,
Tse, H., Mong, K. -L., Li, K. -W., Lam, K. -C. and Yuen, K. -Y.
TITLE Streptococcus dysgalactiae subsp. equisimilis strain ATCC 35666
JOURNAL Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
Pokfulam Road, Hong Kong, China
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ORIGIN

Query Match 68.9%; Score 1128.8; DB 1; Length 1421;
Best Local Similarity 87.2%; Pred. No. 1.5e-220;
Matches 1238; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

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Oy 200 ACATGAGCAAAATTTGCTGTAAGTGGCTTCTTAAGCAAGATGATTTGGTGATG 259
Db 121 ATATGGAGCTAAATTTGCTGTAAGTGGCTTCTTAAGCAAGATGATTTGGTGATG 180
Oy 260 GGACGACTACTGCAACAGTTTGGACCAAGCATTTGCTGTAAGAGCATTAAGATGGA 319

Db 181 GAAACCAACTGCAACAGTATTTGACACAGGCTATCGCTGTAAGGCTTTAAAAATGTA 240
Oy 320 CAGCAGGTGCTATTCATTTGATTCGCTGACGATGTAAGAACACACACAGCAGCTG 379
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Oy 380 TTGAAGCTTGAAGCAACCTTGCATCAACCTGATTTGGCAGGAAGATTTGCTAGTGC 439
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Oy 500 TGGCAACAGTGTGTGATTTACATGCAAGATCTGAGATGTAAGAAAGCAATTTGAG 559
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Oy 980 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1039
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RESULT 10
AX148809 1305 bp DNA Linear PAT 08-JUN-2001
LOCUS AX148809 Sequence 11 from Patent M00136625.
ACCESSION AX148809
VERSION AX148809.1 GI:14347333
KEYWORDS
SOURCE Streptococcus pyogenes.
ORGANISM Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 1305)
AUTHORS Wright, J. A., Young, A. H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences derived from groel and groes as
inhibitors of microorganisms
JOURNAL Patent: WO 0136625-A1 25-May-2001;
Genesense Technologies Inc. (CA)
FEATURES
source 1..1305
location/Qualifiers
BASE COUNT 406 a 238 c 312 g 349 t
ORIGIN

Query Match 68.5%; Score 1122.6; DB 6; Length 1305;
Best Local Similarity 99.2%; Pred. No. 2,7e-219;
Matches 1128; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 11
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LOCUS AY121367 Streptococcus dysgalactiae strain HKU 7, chaperonin GroEL gene, partial cds.
DEFINITION AY121367
ACCESSION AY121367
VERSION AY121367.1 GI:22022493
KEYWORDS
SOURCE Streptococcus dysgalactiae.
ORGANISM Streptococcus dysgalactiae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Moo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. W., Tse, H., Wong, K. L., Li, K. W., Lam, K. C. and Yuen, K. Y.
TITLE Chaperonin GroEL gene of Group G Streptococcus dysgalactiae unpublished
JOURNAL 2 (bases 1 to 1415)
AUTHORS Moo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. W., Tse, H., Wong, K. L., Li, K. W., Lam, K. C. and Yuen, K. Y.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Microbiology, The University of Hong Kong, Pokfulam Road, Hong Kong, China
FEATURES
source 1..1415
location/Qualifiers
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BASE COUNT      404 a      276 c      353 g      382 t
ORIGIN
Query Match      68.3%; Score 1118; DB 1; Length 1415;
Best Local Similarity 86.9%; Pred. No. 2,3e-218;
Matches 1229; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

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LOCUS      AF389514
DEFINITION      Streptococcus bovis GroES gene, complete cds; and GroEL gene,
partial cds.
ACCESSION      AF389514
VERSION      AF389514.1
KEYWORDS      GI:21666288
SOURCE      Streptococcus bovis.
ORGANISM      Streptococcus bovis.
REFERENCE      1 (bases 1 to 2054)
AUTHORS      Teng, L.-J.
TITLE      The groESL genes of Streptococcus bovis
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 2054)
AUTHORS      Teng, L.-J.
TITLE      Direct submission
JOURNAL      Submitted (08-JUN-2001) School of Medical Technology, National
Taiwan University College of Medicine, No. 1, Chang-te Street,
Taipei 100, Taiwan
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BASE COUNT	652 a 361 c 472 g 569 t		
ORIGIN			
Query Match	67.4% Score 1104.2; DB 1; Length 2054;		
Best Local Similarity	80.7% Pred. No. 1.5e-215;		
Matches 1289; Conservative	0; Mismatches 308; Indels 0; Gaps 0;		
OY	1	ATGGCAAAAGAAATCAAAATTTTCAGACAGATGCGCGCTGCTGCTGCGCGAGATTGAT	60
DB	444	ATGGCAAAAGATTAATTTTCAGACAGATGCGCGAGCATGATGCTGCTGCTGAT	503
OY	61	ANGTTCAGATACCGTCAAGTAAAGCTTGCTTAAAGGCGCAATTTGTTCTTGA	120
DB	504	ATTTCGCAATACCGTAAAGTAACTTAGGCGCTAAAGCTCTAACTGTTCTTGA	563
OY	121	AAAGCTTTGCTCCCTTAATTAATTAATGACGGGGTAACCATTCCTAAAGATGAA	180
DB	564	AAATCATTTGCTACCACTTATCAAAATGATGATGACAAATCCCAAGAAATGAA	623
OY	181	TTAGAATCATTTTGAAMACATGAGAGCAAAATGTGTCTGATGCTCTTAAACC	240
DB	624	TTAGAAGACATTTTGAAMATGAGAGCTAACTGTATCAGAGTGTCTTCAAAACA	683
OY	241	AATGATATTGCTGATGATGGGACACTACGACAGATTGTCACACAAACCAATTCAT	300
DB	684	AACGACATCGCTGGTACGTCACAAACGCGCACAGATTTGACAAACCATTCGTTCT	743
OY	301	GAAGCACTTAAATAATGTACAGACAGCGCTAATCCAATTTGGTATCCGTGAGCATGAA	360
DB	744	GAAGCTCTTAAATACTTACGCGGTGCAACCCAAATTTGATACGCTGTGTGATGAA	803
OY	361	ACAGCAACAGACACCTGTGAAGCCTTGAAGCCATTCGCTACCTATCTGCGAC	420
DB	804	TCAGCTGTGCTGTTCATGATGACGAATTAAGATTTGCTCAACCACTGTATATAA	863
OY	421	GAAGTATTGCTCAGTCTGCTGATCATCAGCTCTGAAAAAATGTGAGAGATATATC	480
DB	864	GAGCGATTGCTCAAGTCTGCGGTTTCATCGCTCTGAAAAAATGTGAGATATAT	923
OY	481	TCAGAAGCTATGAGCGGTGTGGGCAAGATGGTGAATTCATCAATCAAAATCTCGAG	540
DB	924	TCAGAAGCTATGAGAAAGTTGGCAAGAGGCTTATACATCTCAAAATCTCGAG	983
OY	541	ATGGAAGCAAGACTTGAAGTGTGAAGGATGCAATTTGACGCTGTACCTGTCA	600
DB	984	ATGGAAGCAAGACTGACCTGTGTGAAGGATGCAATTTGACGCTGTATCTTTCACA	1043
OY	601	TACATGTCTCAGACAAATGATGTTGACAGCTTGAAGAACCATTTATCTTATC	660
DB	1044	TACATGTCTACGACATGAAAAAATGTTGCTGATCTGAAAAATCCATCATCTTGATT	1103
OY	661	ACGGATTAATAAAGTGTCAACATCTCAAGACATTTTGGCACTACTGAGAGATTGATA	720
DB	1104	ACGGATTAAGAAATCTCAACATCTCAAGACATTTTGGCACTACTGAGAGATTGATA	1163
OY	721	ACCAACCTGCATTAATCATTAATTCAGATGATGATGATGATGATGATGATGATGAT	780
DB	1164	ACTATGCTGCATTAATCATTAATTCAGATGATGATGATGATGATGATGATGATGAT	1223
OY	781	GTCTTGACAAAGATTCGTGTGATTTCAATGTGCTGTCTGTCAAGCGCCAGATTGCT	840
DB	1224	GTGCTTAACAAATTCGTGTGATTTCAATGTGCTGTCTGTCAAGCGCCAGATTGCT	1283
OY	841	GATGCTGTAAAGCTATGCTGAAGACATTCATCTTGTGACAGGTGTGATGATGAT	900
DB	1284	GACGCTGTAAAGCAATCTTGAAGATATGCGCTTTAACTGTGTGTGATGATGAT	1343
OY	901	GAGGCTGTAGACTTGAATTAAGATGCTCATATGACAGCCCTTGACAGCTGCTAG	960
DB	1344	GAAAGCTGTGCTTGAATTAAGATGCTCATATGACAGCTTGTGACAGCTGCTAG	1403
OY	961	ATTCACTGTATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1020
DB	1404	GTAATCTGTATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1463
OY	1021	GCTAACCTTATGCTGATTAATGCAATTAAGCAACAACTTGTGACTTGAACCT	1080
DB	1464	GCTATGCTGATATGATTAATTAATGCACTGCAAGCAACAACTGATTAATGACCT	1523
OY	1081	GAATACTAAGAAAGCTTTGGCAATTAAGCTGTGTGTGTGTGTGTGTGTGTGTGT	1140
DB	1524	GAATACTAAGAAAGCTTTGGCTAAATTAAGCTGTGTGTGTGTGTGTGTGTGTGT	1583
OY	1141	GCTCAACAGACAGCTTTAAAGAAATGAAATCGCATGATGAGATGCTGTAAATGCT	1200
DB	1584	GCACCGCACAAAGCAAGATTAAGAAATGAAATCGCATGATGAGATGCTGTAAATGCT	1643
OY	1201	ACAGTGCAGCGCTGAAGAGATATCGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT	1260
DB	1644	ACAGCGCTGCGCTGAAGAGATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1703
OY	1261	ATTGAAAGTGAAGAGCTTTGAGCTGTGAGGCGGATGATGATGATGATGATGATGAT	1320
DB	1704	ATTGAAAGTGTGAGAGCTTTGAGCTGTGAGGCGGATGATGATGATGATGATGATGAT	1763
OY	1321	CTTGCTGCTGTGAAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT	1380
DB	1764	CTTGCTGCTGTGAAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT	1823
OY	1381	GTAATTAATGACAGTTGAAAAACAGCCCTGACAGAACAGATTAATGCTGCAACAGT	1440
DB	1824	GTAATTAATGACAGTTGAAAAACAGCCCTGACAGAACAGATTAATGCTGCAACAGT	1883
OY	1441	GAGTGGTGTGATGATTAAGACAGATCATTTGACCTGTCAAGATGACAGATGACG	1500
DB	1884	GAGTGGTGTGATGATTAAGACAGATCATTTGACCTGTCAAGATGACAGATGACG	1943
OY	1501	CTTCAAAATGACAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT	1560
DB	1944	CTTCAAAATGACAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT	2003
OY	1561	AAACCTGAACAGCTACCGCAGCGCCAGCAATCCAG	1597
DB	2004	CATCCAGAACAGCTGACCCAGCGCCAGCAATCCAG	2040
RESULT 13			
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LOCUS	AY121363	1384 bp	DNA linear BCT 30-JUL-2002
DEFINITION	Streptococcus dysgalactiae subsp. dysgalactiae strain ATCC 43078		
ACCESSION	chaperonin GroEL gene, partial cds.		
	AY121363		

LOCUS AF389516 2324 bp DNA linear BCT 02-JUL-2002
DEFINITION Streptococcus mutans GroES gene, complete cds; and groEL gene,
partial cds.
ACCESSION AF389516
VERSION AF389516.1 GI:21666294
KEYWORDS
SOURCE Streptococcus mutans.
ORGANISM Streptococcus mutans
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE
1 (bases 1 to 2324)
Teng, L.-J.
The groEL genes of Streptococcus mutans
JOURNAL Unpublished
2 (bases 1 to 2324)
Teng, L.-J.
Direct Submission
Submitted (08-JUN-2001) School of Medical Technology, National
Taiwan University College of Medicine, No. 1, Chang-Tse Street,
Taipei 100, Taiwan
FEATURES
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Location/Qualifiers
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BASE COUNT 695 a 368 c 544 g 717 t
ORIGIN
Query Match 65.7%; Score 1075.4; DB 1; Length 2324;
Best Local Similarity 79.8%; Pred. No. 1.1e-209;
Matches 1268; Conservative 0; Mismatches 321; Indels 0; Gaps 0;
QY 1 ATGGCAAGAAATCAATTTTTCAGAGATGCGCGTCCGATGTCGCGGAGATTGAT 60
DB 717 ATGGCAAGAAATCAATTTTTCAGAGATGCGCGTCCGATGTCGCGGAGATTGAT 776
QY 61 ATGTTAGACATACCGTCGAAGTACGCTGCTTAAAGGCGCAATGTTGTTTGA 120
DB 777 ATTTTACAGATACAGTTAAGGTAACTTGGCCCTTAAAGACGCAATGTTGTTTGA 836
QY 121 AAAGCTTTGCTTCCTTAAATTAATGACGGGGTACCATTTGTTAAAGATCGAA 180
DB 837 AAGTCGTTGGTTCACCGCTCATTAATGATGATGTCGTCGTCGTAAGAAATTGA 896
QY 181 TTAGAGATCATTTTGAAGACATGGAGCAAAATTTGTCGAGATGCGCTTAAACC 240
DB 897 TTAGAGATCATTTTGAAGACATGGAGCAAAATTTGTCGAGATGCGCTTAAACC 240
QY 241 AATGATTTGCTGTGATGGAGACTACTGACACGTTTACACAGCATTTGTTTAT 300
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DB 957 AATGATTTGCTGTGATGGAGACTACTGACACGCTTGTACTGACGCTTATTTGCT 1016
QY 301 GAAGACATAAATAATGACAGACAGTCTTATTCATATGTTATGCTGAGCATTTGA 360
DB 1017 GAAGATTTAATAATGCTGTGAGTACACCATGATGATTTGCTGAGCAATGGA 1076
QY 361 ACAGCAACGCAACAGCTGTGTAAGCTTGAAGCCATGCTCAACCTGTATGCGCA 420
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QY 661 ACCGATTAATAATGCTGAACATCCAGACATTTTGGCCTACTTGAAGAGTCTTAA 720
DB 1377 ACCGATTAATAATGCTGAACATCCAGACATTTTGGCCTACTTGAAGAGTCTTAA 1436
QY 721 ACACACGCTCATTAATTAATGACATGATGATGATGATGATGATGATGATGAT 780
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DB 1497 GCTTGAACAGATTCGCTGCTTCAATGATGATGATGATGATGATGATGATGATGAT 1556
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DB 2277 CATCAGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2305

RESULT 15
AF389515 2320 bp DNA linear BCT 02-JUL-2002
LOCUS Streptococcus intermedius GroES gene, complete cds; and GroEL gene,
DEFINITION partial cds.
ACCESSION AF389515
VERSION AF389515.1 GI:21666291
KEYWORDS
SOURCE
ORGANISM Streptococcus intermedius.
Streptococcus intermedius.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 2320)
AUTHORS Teng, L.-J.
TITLE The groESL genes of Streptococcus intermedius
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2320)
AUTHORS Teng, L.-J.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2001) School of Medical Technology, National
Taiwan University College of Medicine, No. 1, Chang-te Street,
Taipei 100, Taiwan

FEATURES
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Location/Qualifiers
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CDS
731 a 408 c 527 g 654 t

BASE COUNT
ORIGIN

Query Match 65 28; Score 1068.2; DB 1; Length 2320;
Best Local Similarity 79.28; Pred. No. 3.2e-208;

Matches 1268; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
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QY 61 ATGTAGCAGATACCGTCAAAAGTAAAGCGTGTCTCAAAAGGCGCATGTGTCTTGA 120
DB 779 ATTTTTCAGATACCGTCAAAAGTAAAGCGTGTCTCAAAAGGCGCATGTGTCTTGA 838
QY 121 AAGCTTTTGTCTCCCTTAATTAATTAAGAGGCGTAAAGGCGCATGTGTCTTGA 180
DB 839 AATATTTTGTCTCCCTTAATTAATTAAGAGGCGTAAAGGCGCATGTGTCTTGA 898
QY 181 TTGAAGATCATTTTGAAGAGGCGTAAAGGCGCATGTGTCTTGA 240
DB 899 CTGCAAGATCATTTTGAAGAGGCGTAAAGGCGCATGTGTCTTGA 958
QY 241 AATGATTTCTGCTGATGAGGAGCTACTGACAGATTTTGACAGAGCATTTGTCAT 300
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DB 1019 GAAGCATTAATAATGTGACAGAGTGTCAATTCGAATTTGTCAGAGCATTTGA 1078
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QY 601 TACATGTGTCAGACATGAAATTAATTTGTCAGAGCTTGAAGCCATTGTCATATTC 660
DB 1319 TACATGTGTCAGACATGAAATTAATTTGTCAGAGCTTGAAGCCATTGTCATATTC 1378
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DB 1379 ACGGATTAATAATGTGTCAGAGCTTGAAGCCATTGTCATATTC 1438
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DB 1558 GATGCTGTCAGATTCGCTGATTTGTCAGAGCTTGAAGCCATTGTCATATTC 1618
QY 901 GAGCATGAGACTTGAATTAAGATGCTACATGACAGCCCTTGACAGGCTGCTAG 960
DB 1619 GAGCATGAGACTTGAATTAAGATGCTACATGACAGCCCTTGACAGGCTGCTAG 1678
QY 961 ATTACAGTGTATGATGACAGATTTGTCAGAGCTTGAAGCCATTGTCATATTC 1020
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QY 1021 GCTAACCGTATGCTGATTAATGCAATTTGAAACAAACACTTGTGACTTACCGT 1080
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OY 1081 GAAAACTACAGACGCTTGGCGAAATAGCTGTGTAGCTGTATCAAGTAGGA 1140
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OY 1141 GCTCCAGAGAGAGAGCTTTAAAAAATGAAATCTCGATTGAGATGCTAAAGCT 1200
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DB 2039 CTTGCTGCTTGGAGAGACAGTGTCAATGCTCAATGAGGATTTGAAGGCTCG 2098
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DB 2099 ATGCTCATTGACGTTGAAAACTGTGAAGTTGGTACAGATTAAATGCTGCAACAGGT 2158
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DB 2159 GAATGGTTAACATGATGAGACAGGAGATCATGACCCAGTCAAAAGTCACTGTTCTGCC 2218
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DB 2219 CTTCAAAATGCTGCTGATGACTAGCTTATTTTAAACACAGACAGCACTTGTGCTAGC 2278
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DB 2279 CAACCGAAGACGCTAGCCAGCTCCGCAATGGATCCAG 2319
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Search completed: April 15, 2003, 03:00:14
Job time : 438.53 secs